如果我们的有效的,我们也有的,我们也有的的,我们的一个,我们的一个,我们的一个,我们的一个,我们的一个,我们的一个,我们的一个,我们的一个,我们的一个,我们的一个, (MT)

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MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

lar output not generated. Thu Oct 21 16:29:45 1999; MasPar time 4.57 Seconds 519.801 Million cell updates/sec

Description: Perfect Score: Sequence:

Title: >US-08-978-217-7 (1-84) from US08978217.pep 599

1 NCALEELRLYFGPLGDQLHA.....ELLDDGQQASPYHPGSCGAG 84

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37. 1:swissprot

Statistics: Mean 41.198; Variance 80.907; scale 0.509

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sult	Score	Query Match	Length	DB	ID	Description	Pred. No.
-	98	16.4	174	٠.	GSPM_PSEAE	GENERAL SECRETION PATH	1.00e-01
N	94	15.7	277	<u>, , , , , , , , , , , , , , , , , , , </u>		E PROTEASE	3.43e-01
w	94	15.7	364	μ.	YBBB_ECOLI	HYPOTHETICAL 41.1 KD P	3.43e-01
4	91	15.2	958	<u>س</u>	SYAC_YEAST	ALANYL-TRNA SYNTHETASE	8.45e-01
S	91	15.2	2870	Ь	NDVB_RHIME	319 KD PROTEIN.	
6	89	14.9	395	ب	APA4_MOUSE	APOLIPOPROTEIN A-IV PR	1.52e+00
7	89		916	ᆫ	SECA_TREPA	PREPROTEIN TRANSLOCASE	1.52e+00
œ	89	14.9	952	_	IF41_YEAST	EUKARYOTIC INITIATION	1.52e+00
9	88	14.7		_	YGFB_ECOLI	HYPOTHETICAL 21.5 KD P	2.04e+00
10	88	14.7	241	ب	RPEP_ALCEU	RIBULOSE-PHOSPHATE 3-E	
11	88	14.7	2418	ب	SPCA_HUMAN	SPECTRIN ALPHA CHAIN,	
12	86	14.4	183	ب	YDJA_ECOLI	HYPOTHETICAL 20.1 KD P	3.63e+00
13	86	14.4	308	_	GRP3_ARTSA	GLYCINE-RICH PROTEIN G	3.63e+00
14	86	14.4	317	_	APE_PIG	APOLIPOPROTEIN E PRECU	
15	85	14.2	202	_	SODM_RABIT	SUPEROXIDE DISMUTASE [4.82e+00
16	85	14.2	289	ᆫ	RMLA_STRMU	GLUCOSE-1-PHOSPHATE TH	4.82e+00
17	85	14.2	341	,	NU2M_ANOGA	NADH-UBIQUINONE OXIDOR	4.82e+00
18	85	14.2	341	<u>, , , , , , , , , , , , , , , , , , , </u>	NU2M_ANOQU	NADH-UBIQUINONE OXIDOR	4.82e+00
19	85	14.2	348	ب	NU2M_LATCH	NADH-UBIQUINONE OXIDOR	4.82e+00
20	85	14.2	655	سر	PARE_BACSU	TOPOISOMERASE IV SUBUN	4.82e+00
21	85	14.2	785	-	CUL3_SCHPO	CULLIN HOMOLOG 3 (CUL-	4.82e+00
22	85	14.2	807	۳,	OXYB_HUMAN	OXYSTEROL-BINDING PROT	4.82e+00
23	85	14.2	809	_	OXYB_RABIT	OXYSTEROL-BINDING PROT	4.82e+00

45	44	43	42	41	40	39	38	37	36	35	ω A	33	32	31	30	29	28	27	26	25	24
82	82	82	82	82	82	82	82	82	83	83	83	83	83	84	84	84	84	84	84	84	85
13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.9	13.9	13.9	13.9	13.9	14.0	14.0	14.0	14.0	14.0	14.0	14.0	14.2
1168	864	658	568	274	274	222	222	166	1469	896	868	249	101	1220	942	351	341	341	274	187	849
_	μ	μ.	ه	_	ب	ب	ب	_	ب	<u>ب</u>	H	ᆫ	_	,_	ᆫ	۲	ب	_		 4	ب
DDX8_SCHPO	ALKS_PSEOL	SPEA_ECOLI	MEND_HAEIN	NU2M_DROSI	NU2M_DROSE	SODM_MOUSE	SODM_HUMAN	VG17_BPPH2	DP27_CAEEL	EP15_HUMAN	NI80_YEAST	EIA_ADE40	YDHR_ECOLI	DDX8_HUMAN	DPO1_CHLAU	COTS_BACSU	NU2M_DROME	NU2M_DROYA	NU2M_DROMA	OX4L_RABIT	FSC1_MOUSE
PUTATIVE PRE-MRNA SPLI	REGULATORY PROTEIN ALK	BIOSYNTHETIC ARGININE	2-SUCCINYL-6-HYDROXY-2	NADH-UBIQUINONE OXIDOR		SUPEROXIDE DISMUTASE [SUPEROXIDE DISMUTASE [EARLY PROTEIN GP17.	CHROMOSOME CONDENSATIO	EPIDERMAL GROWTH FACTO	NIP80 PROTEIN (NIP100	EARLY E1A 27 KD PROTEI	HYPOTHETICAL 11.3 KD P	PROBABLE ATP-DEPENDENT	DNA POLYMERASE I (EC 2	SPORE COAT PROTEIN S (NADH-UBIQUINONE OXIDOR		NADH-UBIQUINONE OXIDOR	OX40 LIGAND (OX40L).	MAJOR FIBROUS SHEATH P
1.11e+01	1.11e+01	1.11e+01	1.11e+01	1.11e+01	1.11e+01	,1.11e+01		1.11e+01				8.44e+00		٠		6.39e+00	6.39e+00	6.39e+00	6.39e+00	6.39e+00	4.82e+00

ALIGNMENTS

RESULT

						•																							
Qy Qy	Ma B Q	SO	₹ :	DR DR	DR	88	36	38	ន	36	3 6	88	88	ဌ	3 8	4 2	R	RA	RX	RP	2 8	88	SO	GN	DE	DT.	DŢ	D.	Αij
98 AALQGMVTASAAQAGLSVERLDNEGEGAVQVALQPAPFAKLLPWLEQLNGQGVQVA 153 : : : : : :	Query Match 16.4%; Score 98; DB 1; Length 174; Best Local Similarity 30.4%; Pred. No. 1.00e-01; Matches 17; Conservative 17; Mismatches 21; Indels 1; Gaps 1;	TRANSMEM 33 52 POTENTIAL. SEQUENCE 174 AA; 19265 MW; 2160BB8F CRC32;	T; TRANSMEMBRANE; INN	PIR; S12356; S12356. PIR: S21639; S21639.	; X56183;	@isb-sib.ch).	requires a license agreement (See ht	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial	the European Bioinformatics Institute. There are no restrictions on its	hetween the Swiss Institute of Bioinformatics and the EMBL outstation -	This court is a constant of the produced through a collaboration	BELONGS TO THE EXEM/PULM/OUTM/	- - SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).	EXPORT OF PROTEINS.	-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE	OUTER MEMDIANE INVOLVES COMMON MECHANISMS IN OTFICER PACKETIA. ,		FILLOUX A., BALLY M., BALL G., AKRIM M., TOMMASSEN J., LAZDUNSKI A.;	91092255.	SEQUENCE FROM N.A.	[1]	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;		XCPZ.	RETION PATH	(REL. 32, LAST	(REL. 22,	1992 (REL.	GSPM_PSEAE STANDARD; PRT; 174 AA. P25061: